

1

Figure 1A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

```
1 TACTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACCATGCAGCTCCCACT
51 GGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCCGTGTAGTGG
101 AGGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCACGGAAATCATCCCC
151 GAGCTCGGAGAGTACCCCGAGCCTCCACCGAGCTGGAGAACAAACAAGAC
201 CATGAACCGGGCGGAGAACGGAGGGCGGCCTCCCCACCACCCCTTTGAGA
251 CCAAAGACGTGTCCGAGTACAGCTGCCGCGAGCTGCACTTCACCCGCTAC
301 GTGACCGATGGGCCGTGCCGCGAGCGCCAAGCCGGTCACCGAGCTGGTGTG
351 CTCCGGCCAGTGCAGCCCGGCGCGCCTGCTGCCAACGCCATCGGCCGCG
401 GCAAGTGGTGGCGACCTAGTGGGCCCGACTTCGCTGCATCCCCGACCGC
451 TACCGCGCGCAGCGCGTGCAGCTGCTGTGTCCCGGTGGTGAGGCGCCGCG
501 CGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCAAGCGCCTCACCC
551 GCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCGG
601 CCGCAGAAGGGCCGGAAGCCGCGGCCCGCGCCCGGAGCGCCAAAGCCAA
651 CCAGGCCGAGCTGGAGAACGCCTACTAGAGCCCGCCCGCGCCCCCTCCCA
701 CCGGCGGGCGCCCCGCCCTGAACCCGCGCCCCACATTTCTGTCTCTGC
751 GCGTGGTTT
```

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

```
1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRPPHHPFETK
51 DVSEYSCRELHFTRYVTDGPCRSAPVTELVCSGQCGPARLLPNAIGRGK
101 WWRPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRF
151 HNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAY
```

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

```
1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATEIIPELGEYPEPPPEL
51 ENNKTMNRAENGGRPPHHPFETKDVSSEYSCRELHFTRYVTDGPCRSAPV
101 TELVCSGQCGPARLLPNAIGRGKWWRPSGPDFRCIPDRYRAQRVQLCPG
151 GEAPRARKVRLVASCKCKRLTRFHQNQSELKDFGTEAARPQKGRKPRPRAR
201 SAKANQAELENAY
```

2

Figure 2A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

```
1 ATGCAGCCCTCACTAGCCCCGTGCCTCATCTGCCTACTTGTGCACGCTGC
51 CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA
101 CAGAGGTCACTCCAGGGCTTGGAGAGTACCCCGAGCCTCCTCTGAGAAC
151 AACCAGACCATGAACCGGGCGGAGAATGGAGGCAGACCTCCCCACCATCC
201 CTATGACGCCAAGATGTGTCCGAGTACAGCTGCCGCGAGCTGCACTACA
251 CCCGCTTCTCTGACAGACGGCCCATGCCGCGAGCGCAAGCCGGTCACCGAG
301 TTGGTGTGCTCCGGCCAGTGC GGCCCCCGCGCGGCTGCTGCCCAACGCCAT
351 CGGGCGCGTGAAGTGGTGGCGCCCGAACGGACCGGATTTCGCTGCATCC
401 CGGATCGCTACCGCGCGCAGCGGGTGCAGCTGCTGTGCCCGGGGGCGCG
451 GCGCCGCGCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAAGTGCAAGCG
501 CCTCAGCCGCTTCCACAACCAAGTCGGAGCTCAAGGACTTCGGGCGGAGA
551 CCGCGCGGCCGAGAAGGGTCGCAAGCCGCGGCCCGGCGCCCGGGGAGCC
601 AAAGCCAACCAGGCGGAGCTGGAGAACGCCTACTAG
```

B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

```
1 QGWQAFRNDATEVIPGLGEYPEPPPENQTMNRAENGGRPPHHPYDAKDV
51 SEYSCRELHYTRFLTDGPCRSAPVTELVCSGQCGPARLLPNAIGRVKWW
101 RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHN
151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY
```

C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

```
1 MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
51 NQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAPVTE
101 LVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPGGA
151 APRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGA
201 KANQAELENAY
```

### Figure 3

GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213  
to: Mouse Cloaked-2 check: 9489 from: 1 to: 211

Symbol comparison table:  
/GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp  
CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1028	Length:	213
Ratio:	4.872	Gaps:	1
Percent Similarity:	91.469	Percent Identity:	88.152

Match display thresholds for the alignment(s):  
| = IDENTITY  
: = 2  
. = 1

Human Cloaked-2 (SEQ ID NO: 5) x  
Mouse Cloaked-2 (SEQ ID NO: 6)

```

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL 50
  || || |:|||| || ||||| |:| |:| |||||
1 MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPP.. 48

51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPV 100
  |||.|||||::: ||||| |:| |:| |||||
49 ENNQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTGDGPCRSAKPV 98

101 TELVCSGQCQGPAPLLPNAIGRGKWWRPSPGDFRCIPDRYRAQRVQLLCPG 150
  ||||| |||||. ||||| ||||| |||||
99 TELVCSGQCQGPAPLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPG 148

151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR 200
  | |||. ||||| ||||| ||||| ||||| |||||
149 GAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGAR 198

201 SAKANQAELENAY 213
  |||||
199 GAKANQAELENAY 211
  
```

GAP of: Human Cloaked-1 check: 1888 from: 1 to: 183  
to: Human Cloaked-2 check: 185 from: 1 to: 190

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003

```

      Quality:      335
      Ratio:       1.831
Percent Similarity: 52.542
      Length:      196
      Gaps:        6
Percent Identity:  42.938

```

```
Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1
```

Human Cloaked-1 (SEQ ID NO: 25) x  
Human Cloaked-2 (SEQ ID NO: 2)

```

1 .....FKNDATEILYSHVVKP.VPAHPSSNSTLNQARNGGRHFSNTGLDR 44
  |||||: | | | | | | |
1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRP.PHPFET 49
  .
45 NTRVQVGCRELRSTKYISDGOCTSISPLKELVCAGECLPLPVLPNWIGGG 94
  : |||| | : | : . | | | . ||| | | |
50 KDVSEYSCRELHFTRYVTDGPCRSAPVTELVCSGQCGPARLLPNAIGRG 99
  .
95 YGKYWSRRSSQEWRCVNDKTRTORIQLQCQDG.STRTYKITVVTTACKCK 143
  | : | | | : . | | : | : | | | | . | | : . | : |||
100 ...KWW.RPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCK 145
  .
144 RYTRQHNNESSHNFESMSPAKPVQHHREKRASKSSKHSMS..... 183
  | || ||| : | | : | | | : | . | .
146 RLTRFHNQSELKDFGTEAAPQOKGRKPRPRA.RSAKANQAELENAY 190

```